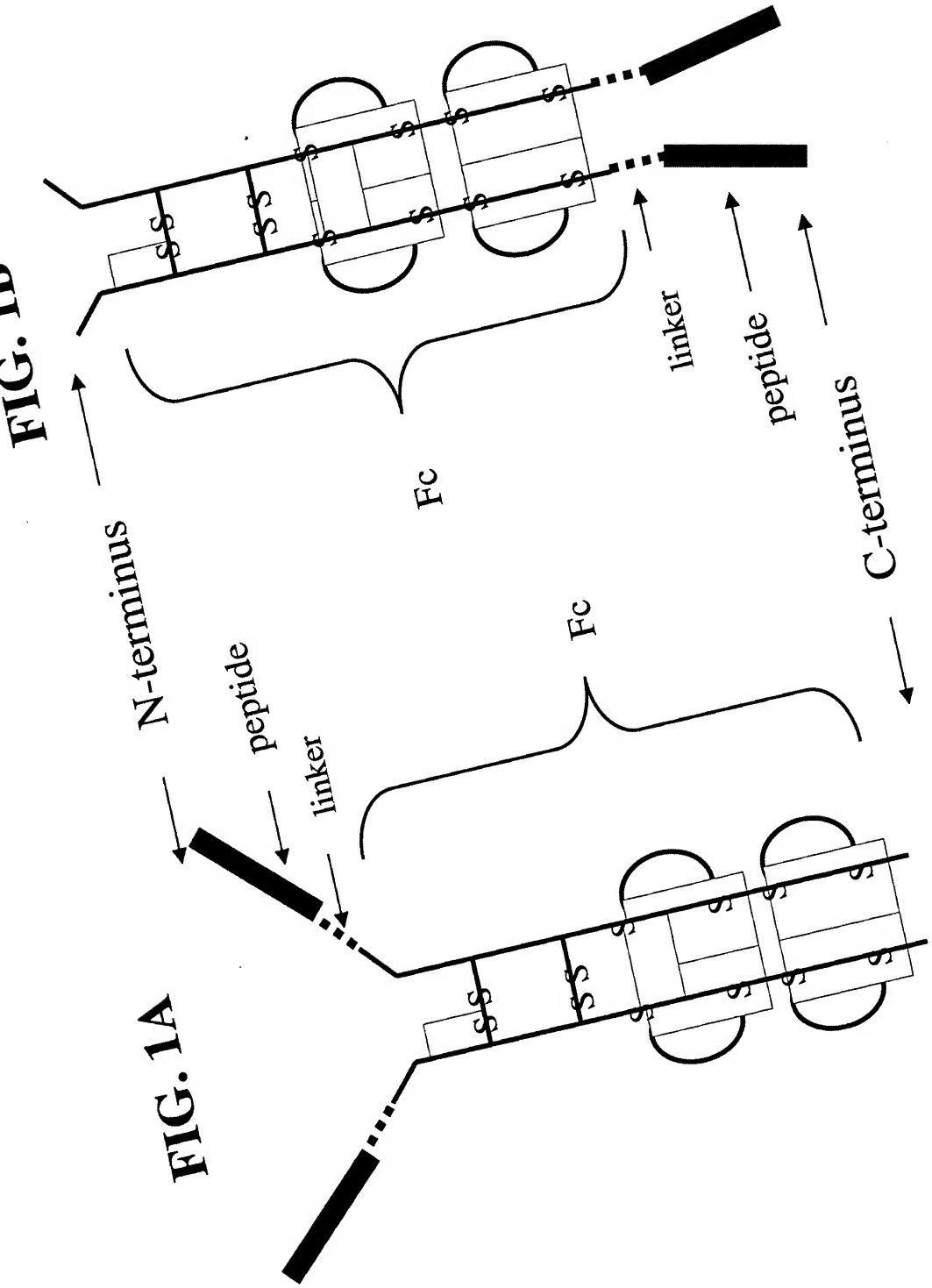

N-terminus
peptide
linker
Fc
linker
peptide
C-terminus
S S
S S

FIG. 1A

FIG. 1B

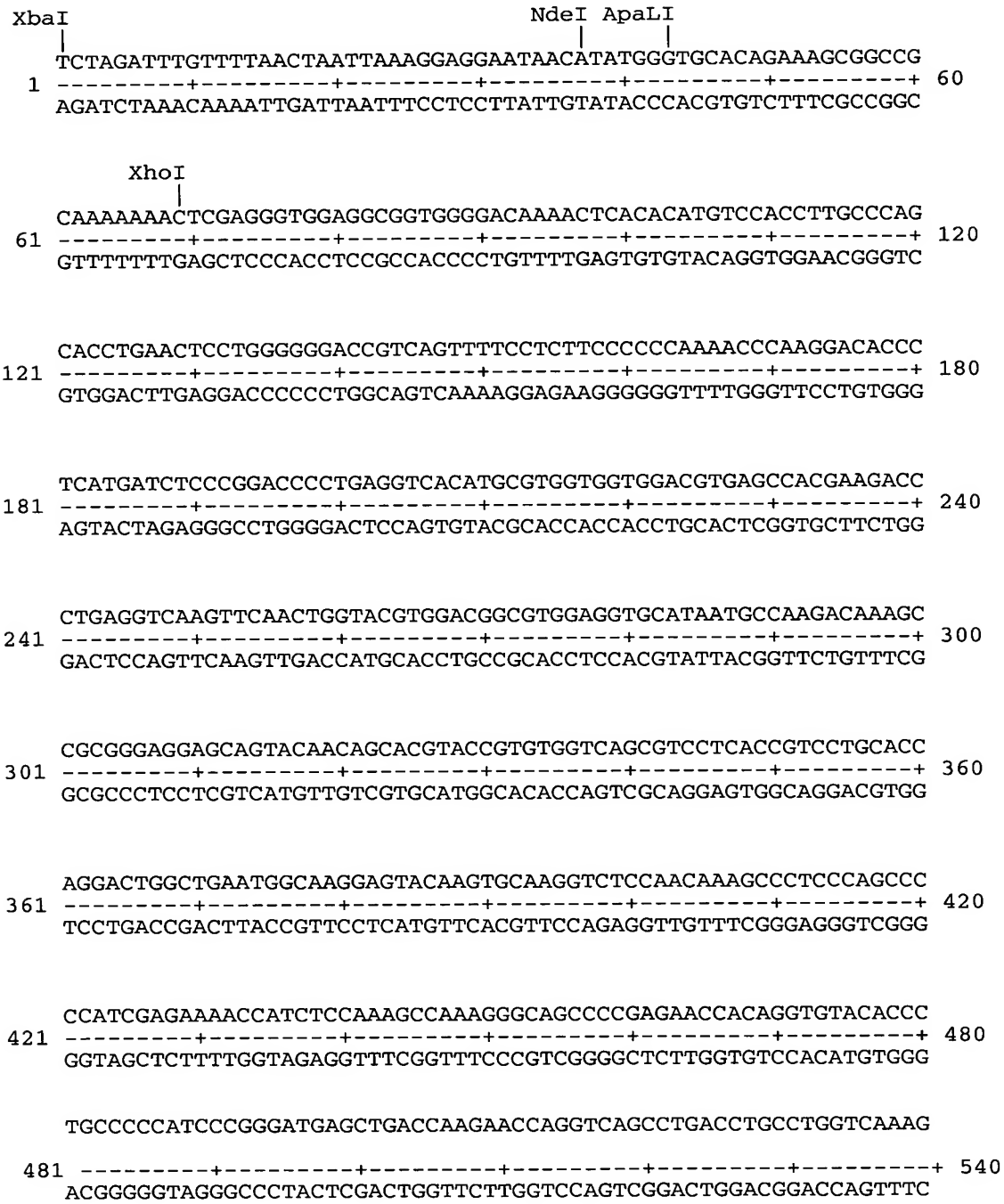
FIG. 2A

```
   ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA
 1 ---------+---------+---------+---------+---------+---------+ 60
   TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

   M  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S

   GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61 ---------+---------+---------+---------+---------+---------+ 120
   CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

   V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V

   ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 ---------+---------+---------+---------+---------+---------+ 180
   TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

   T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V

   GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 ---------+---------+---------+---------+---------+---------+ 240
   CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

   D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T

   TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 ---------+---------+---------+---------+---------+---------+ 300
   ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG

   Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y

   AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 ---------+---------+---------+---------+---------+---------+ 360
   TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

   K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A

    AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 ---------+---------+---------+---------+---------+---------+ 420
   TTTCCCGTCGGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

   K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  T

   AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 ---------+---------+---------+---------+---------+---------+ 480
   TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

   K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V
```

FIG. 2B

```
    GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
481 ---------+---------+---------+---------+---------+---------+ 540
    CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG

    E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D

    TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 ---------+---------+---------+---------+---------+---------+ 600
    AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

    S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q

    GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 ---------+---------+---------+---------+---------+---------+ 660
    CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

    G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K

    AGCCTCTCCCTGTCTCCGGGTAAA
661 ---------+---------+----  684
    TCGGAGAGGGACAGAGGCCCATTT

    S  L  S  L  S  P  G  K
```

FIG. 3A


XbaI
NdeI ApaLI
XhoI
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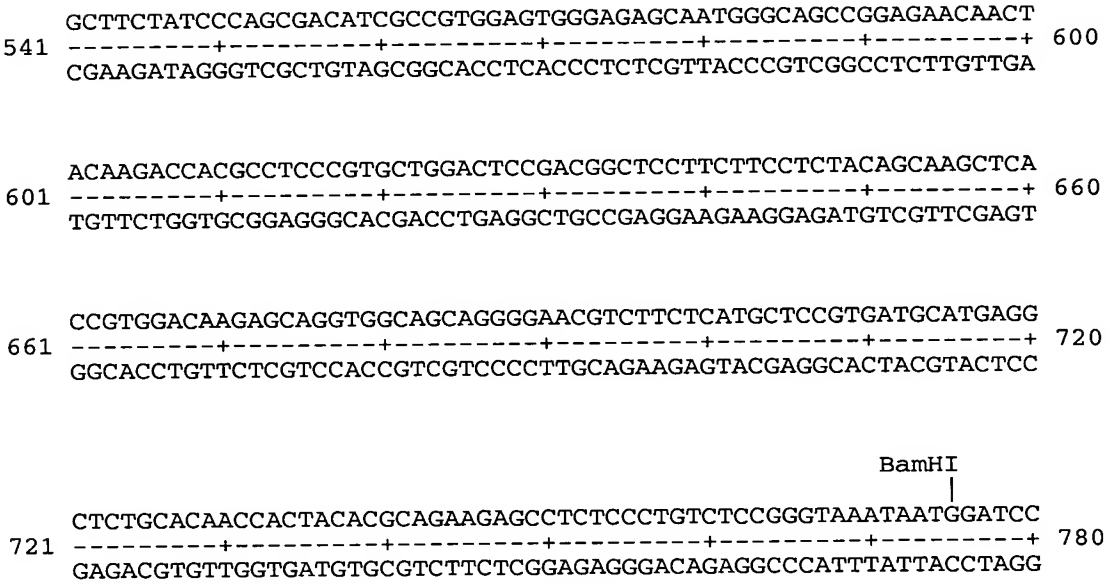
CAAAAAAACTCGAGGGTGGAGGCGGTGGGGACAAAACTCACACATGTCCACCTTGCCCAG
GTTTTTTTGAGCTCCCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTC
CACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCC
GTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGG
TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC
AGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGG
CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC
GACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCG
CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC
GCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGG
AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
TCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGG
CCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCC
GGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGG
TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
ACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTC
1
61
121
181
241
301
361
421
481
60
120
180
240
300
360
420
480
540

FIG. 3B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541
600
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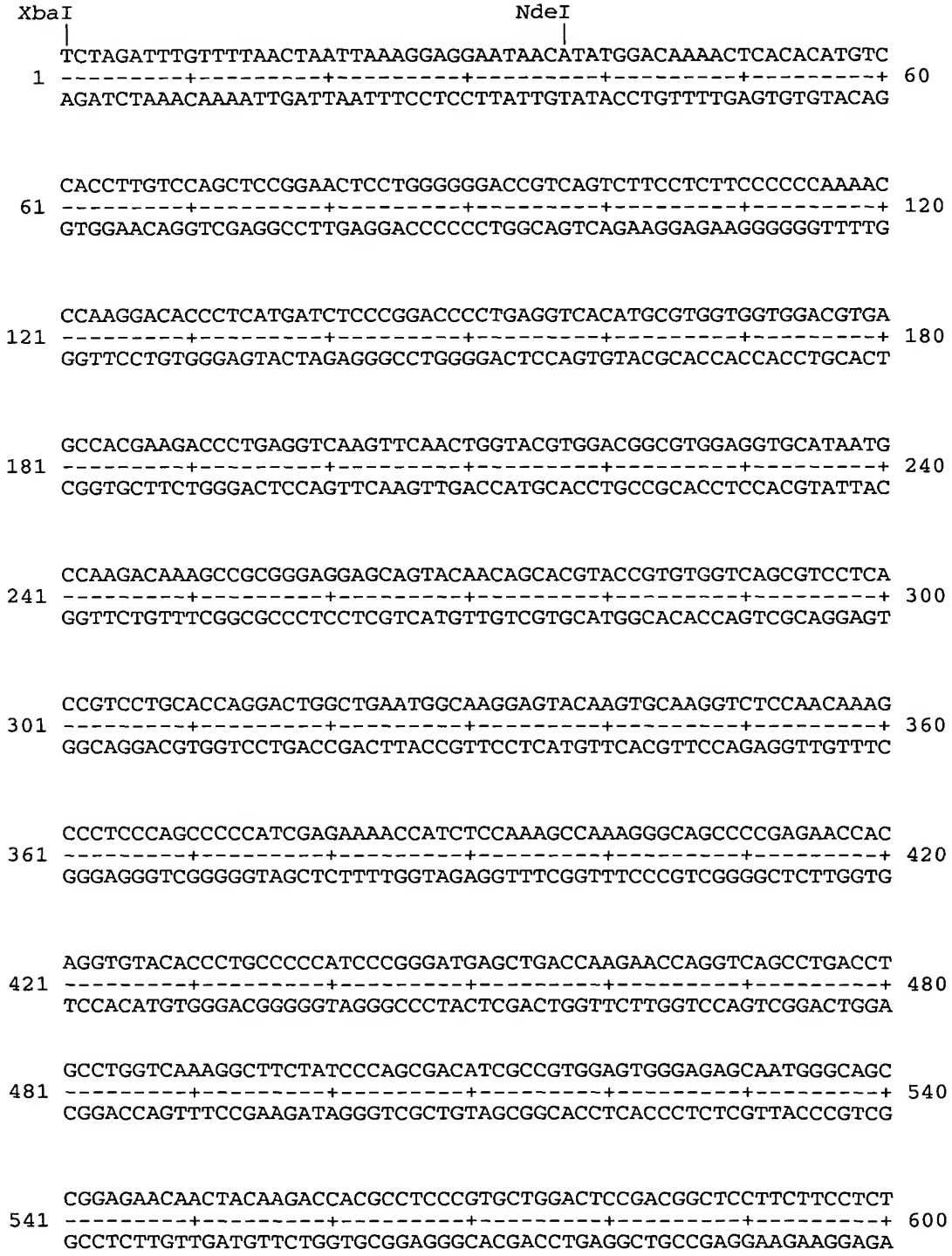
ACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCA
601
660
TGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT
CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
661
720
GGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCC
BamHI
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721
780
GAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

FIG. 4A


XbaI
NdeI
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AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
1
60
CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
61
120
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
121
180
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
181
240
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
241
300
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
301
360
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
361
420
AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
421
480
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
481
540
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
541
600

FIG. 4B

```
    ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601 ---------+---------+---------+---------+---------+---------+ 660
    TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC

    TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
661 ---------+---------+---------+---------+---------+---------+ 720
    ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT

              ApaLI                          XhoI      BamHI
                |                              |         |
    AAGGTGGAGGTGGTGGTGCACAGAAAGCGGCCGCAAAAAAACTCGAGTAATGGATCC
721 ---------+---------+---------+---------+---------+-------- 777
    TTCCACCTCCACCACCACGTGTCTTTCGCCGGCGTTTTTTTGAGCTCATTACCTAGG
```

FIG. 5

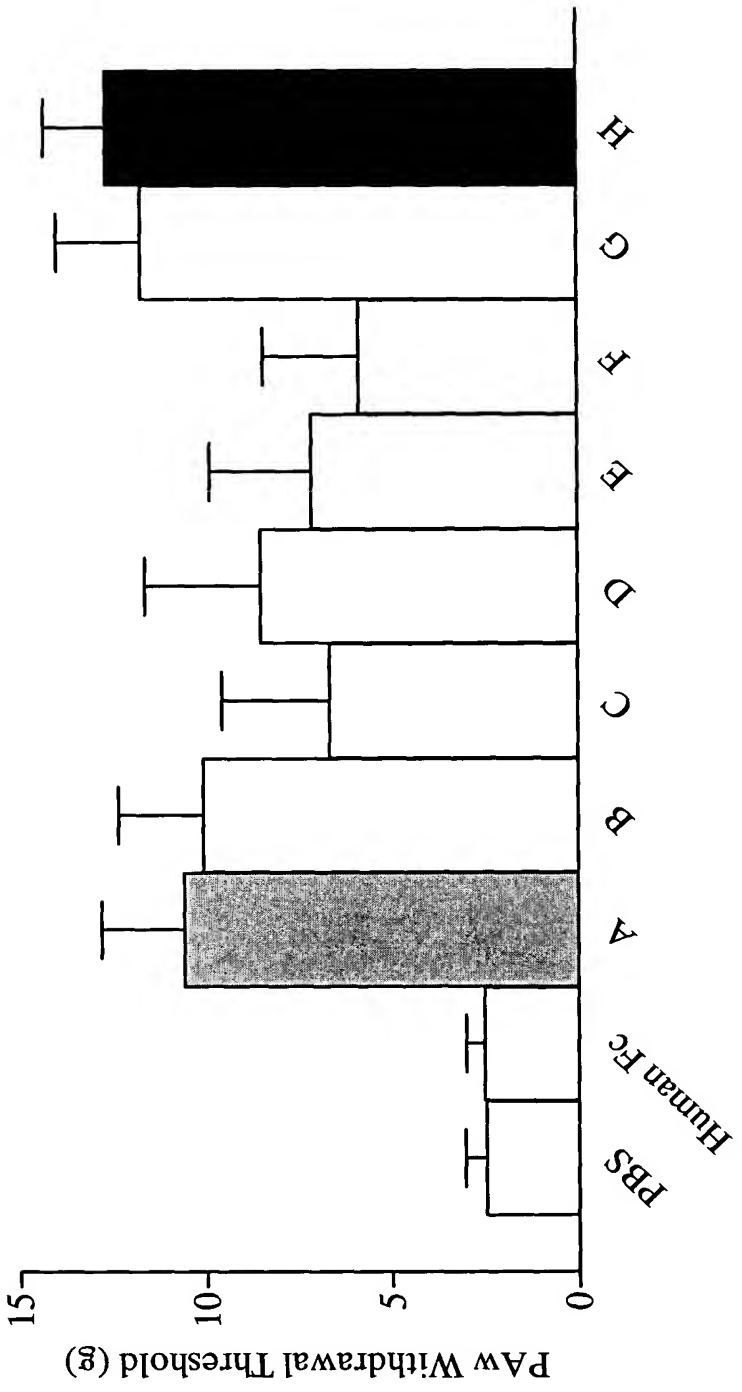

FIG. 6